



SEQUENCE LISTING

<110> HUGANIR, RICHARD L.
KIM, GJEEHAE

<120> SIGNAL TRANSDUCING SYNAPTIC MOLECULES AND USES THEREOF

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<140> 09/294,298
<141> 1999-04-19

<150> 60/082,690
<151> 1998-04-22

<150> 60/082,717
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<160> 21

<170> PatentIn Ver. 2.1

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SYNGAP-A

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Thr Gln Tyr Val His Ser Pro Tyr Asp Arg Pro Gly Trp Asn Pro Arg
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ttc tgc atc atc tct ggg aac cag ctg ctc atg ctg gat gag gat gag 144
Phe Cys Ile Ile Ser Gly Asn Gln Leu Leu Met Leu Asp Glu Asp Glu
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ata cac ccc ctt ctg atc cgc gac cgg agg agc gag tcc agc cga aac 192
Ile His Pro Leu Leu Ile Arg Asp Arg Arg Ser Glu Ser Ser Arg Asn
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Lys Leu Leu Arg Arg Thr Val Ser Val Pro Val Glu Gly Arg Pro His
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Val	Arg	Ala	Leu	Arg	Leu	His	Leu	Tyr	Arg	Asp	Ser	Asp	Lys	Lys	Arg		
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Lys	Lys	Asp	Lys	Ala	Gly	Tyr	Val	Gly	Leu	Val	Thr	Val	Pro	Val	Ala		
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Cys	Ala	Val	Leu	Glu	Pro	Ala	Leu	Asn	Val	Lys	Gly	Lys	Glu	Glu	Val		
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Phe	Leu	Ser	Asp	Met	Ala	Met	Ser	Glu	Val	Asp	Arg	Phe	Met	Glu	Arg		
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gaa	ca	ct	at	tt	cg	ga	aa	ac	cg	ct	gc	act	aa	g	ca	1440	
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Glu	Phe	Ile	Arg	Ala	Leu	Tyr	Glu	Ser	Glu	Glu	Asn	Cys	Glu	Val	Asp		
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Cys Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile Ser Ala	
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Ser Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro Ser Leu	
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Phe Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg Thr Leu	
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Glu Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn Leu Asp	
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cgc cag agc gag cgc gct cgg tct cag ccc atg gtgtctgcgc ggg ccg	2208
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Ser Ala Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser Ser Ile	
740 745 750	

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Lys Ile Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu Lys Arg				
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Gly Arg Leu Met Leu Val Glu Glu Leu Arg Arg Asp His Pro Ala				
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Arg Gly Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val Arg Trp				
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Pro His Leu Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro				
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Ser Pro Pro Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro Tyr Pro Gly				
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Ser Pro Thr Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser				
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Pro Leu Thr Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His				
tcc agg agg gag agt ggg acc ctc agc tgc cct ctc acc cca gga cac	1395	1400	1405	4224
Ser Arg Arg Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr Pro Gly His				
cac cta ccc cac aca gac ccc ttc act ctg ggg tgc tat ccc cat cct	1410	1415	1420	4272
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 <223> Description of Unknown Organism: mammalian
 SYNGAP-A

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 Ile His Pro Leu Leu Ile Arg Asp Arg Arg Ser Glu Ser Ser Arg Asn
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 Lys Leu Leu Arg Arg Thr Val Ser Val Pro Val Glu Gly Arg Pro His
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 Gly Glu His Glu Tyr His Leu Gly Arg Ser Arg Arg Lys Ser Val Pro
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 Gly Gly Lys Gln Tyr Ser Met Glu Ala Ala Pro Ala Ala Pro Phe Arg
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 Pro Ser Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile Lys Arg
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 Thr Lys Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg Gln Ile
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 Leu Pro Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu Met Gln
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 Ser Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser
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 Ala Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Ile Lys
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 Pro Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr
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 Thr Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg
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 Asp Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp
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 Ala Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu Thr Ala
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Ala Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln Gly Ser
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 Ile Glu Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys Glu Tyr
 1155 1160 1165

Ser Lys Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu Tyr Glu
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 Glu Glu Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn Arg Lys
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 Leu Glu Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln Thr Ser
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 Lys Ile Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu Lys Arg
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 Leu Arg Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser Ile Ile
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 1250 1255 1260
 Met Ala Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp Ala Gln
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 Arg Gly Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val Arg Trp Pro
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 His Leu Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro Gly
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 Pro Thr Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser Pro
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 Leu Thr Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His Ser
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SYNGAP-B

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tgc ccc ctc ctt ccc acc gcc agc ctc tcc gcc gcc gct gct ctt cct				96
Cys Pro Leu Leu Pro Thr Ala Ser Leu Ser Ala Ala Ala Leu Pro				
20 25 30				
gct gct ttc cgg ggg aat acc act tgg gtc gct cga gga gga aga gtg				144
Ala Ala Phe Arg Gly Asn Thr Thr Trp Val Ala Arg Gly Arg Val				
35 40 45				
tcc ccg ggg ggg aaa cag tac agc atg gaa gcc gcc ccc gct gcg ccc				192
Ser Pro Gly Gly Lys Gln Tyr Ser Met Glu Ala Ala Pro Ala Ala Pro				
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Phe Arg Pro Ser Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile				
65 70 75				
aaa cgt aca aag tca caa ccc aaa ctt gac cgg acc agc agc ttt cga				288
Lys Arg Thr Lys Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg				
80 85 90 95				
cag atc ctg cct cgc ttc cga agt gct gac cat gac cgg gcc cgg ctg				336
Gln Ile Leu Pro Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu				
100 105 110				
atg cag agc ttc aag gag tct cac tcc cat gag tcc ctg ctg agt ccc				384
Met Gln Ser Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro				
115 120 125				
agc agt gct gag gcc ctg gag ctc aac ctg gat gaa gac tcc att				432
Ser Ser Ala Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile				
130 135 140				
atc aag cca gta cac agc tcc atc ctg ggc cag gag ttc tgc ttt gag				480
Ile Lys Pro Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu				
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Val Thr Thr Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala				
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gaa agg gac aaa tgg att gag aat cta cag agg gct gtg aaa ccc aac				576
Glu Arg Asp Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn				
180 185 190				
aag gac aac agc cgc cgg gta gat aac gtg ctg aaa cta tgg atc ata				624
Lys Asp Asn Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile				
195 200 205				

gaa gct cga gag ctg ccc ccc aag aag cga tat tac tgc gag tta tgc Glu Ala Arg Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys 210 215 220	672
ctg gac gac atg ctc tat gca cgg acc act tcc aag ccc cgc tca gcc Leu Asp Asp Met Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala 225 230 235	720
tca gga gac act gtc ttt tgg ggc gag cac ttc gag ttt aac aac ctg Ser Gly Asp Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu 240 245 250 255	768
cct gct gtc cgg gcg ctg cgg ctg cat ctg tac cgt gac tcg gac aaa Pro Ala Val Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys 260 265 270	816
aag cgg aag aag gac aag gca ggc tac gtt ggc ctg gtg act gtt cca Lys Arg Lys Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro 275 280 285	864
gtg gcc acc ctg gct ggg cgc cac ttc aca gag cag tgg tac ccc gtg Val Ala Thr Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val 290 295 300	912
acc ctg cca aca gga agt ggg ggc tct ggg ggt atg ggc tcg ggg gga Thr Leu Pro Thr Gly Ser Gly Ser Gly Gly Met Gly Ser Gly Gly 305 310 315	960
gga ggg ggg tca ggg ggc tca ggg ggc aaa ggg aaa gga ggc tgt Gly Gly Ser Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys 320 325 330 335	1008
cct gct gtg cgg ctg aag gcc cgt tac cag aca atg agt atc ctg ccc Pro Ala Val Arg Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro 340 345 350	1056
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atg ctg tgt gcc gtg ctg gag ccc gcc ctc aat gtc aag ggc aag gag Met Leu Cys Ala Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu 370 375 380	1152
gag gtc gct agt gca ctg gtt cac atc ctg caa agc aca ggc aag gcc Glu Val Ala Ser Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala 385 390 395	1200
aag gac ttc ctt tca gac atg gcc atg tca gag gta gac cgg ttc atg Lys Asp Phe Leu Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met 400 405 410 415	1248
gag cgg gaa cac ctc ata ttc cgc gag aac acg ctc gcc act aaa gcc Glu Arg Glu His Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala 420 425 430	1296

ata gaa gag tat atg aga ctg att ggc cag aaa tac ctc aag gat gcc Ile Glu Glu Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala 435 440 445	1344
att ggg gag ttc atc cgg gct ctg tat gaa tct gag gag aac tgt gaa Ile Gly Glu Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu 450 455 460	1392
gta gac ccc atc aag tgc aca gcg tcc agt ctg gca gag cac cag gcc Val Asp Pro Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala 465 470 475	1440
aac ctg cgg atg tgc tgt gag ttg gcc ctg tgc aag gtg gtc aac tcc Asn Leu Arg Met Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser 480 485 490 495	1488
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agt ctg ttt gga ctg atg cag gag tac cca gat gag cag acc tca cga Ser Leu Phe Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg 545 550 555	1680
acc ctc acc ctc atc gcc aag gtt atc cag aac ctg gcc aac ttt tcc Thr Leu Thr Leu Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser 560 565 570 575	1728
aag ttt acc tca aag gag gac ttc ctg ggc ttc atg aac gag ttt ctg Lys Phe Thr Ser Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu 580 585 590	1776
gag ctg gag tgg ggt tct atg cag caa ttc ttg tat gag ata tcc aac Glu Leu Glu Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn 595 600 605	1824
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cag ctc agc aag gaa gcc ctc ctg aag ctg ggc ccg ctg ccc cgg ctc Gln Leu Ser Lys Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu 640 645 650 655	1968

ctc agc gac atc agc aca gcc ctg agg aac cct aac atc caa agg cag Leu Ser Asp Ile Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln 660 665 670	2016
ccg agc cgc cag agc gag cgc gct cgg tct cag ccc atg gtg ctg cgc Pro Ser Arg Gln Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg 675 680 685	2064
ggg ccg tca gcc gag atg cag ggc tac atg atg cgg gac ctc aac agc Gly Pro Ser Ala Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser 690 695 700	2112
tcc atc gac ctt cag tcc ttc atg gct cga ggc ctc aac agc tct atg Ser Ile Asp Leu Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met 705 710 715	2160
gac atg gct cgc ctc ccc tcc cca acc aag gag aaa ccc ccc ccc ccc Asp Met Ala Arg Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro 720 725 730 735	2208
cct ccc ggt ggg ggt aaa gac ctg ttc tat gtg agc cgg cca cca ctg Pro Pro Gly Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu 740 745 750	2256
gcc cggtcc tcc cca gca tac tgc acg agc agc tcg gac atc aca gag Ala Arg Ser Ser Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu 755 760 765	2304
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aac ctg gca gct gtt ggg gac ctg ttg cac tca agc cag gct tca ctg Asn Leu Ala Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu 800 805 810 815	2448
aca gca gcc ttg ggg ttg cgg cct gca cct gcc ggg cgc ctc tcc caa Thr Ala Ala Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln 820 825 830	2496
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ggt gtc act acg gat ggt gtc ccc gcc cag caa ctg cgc atc cct ctt Gly Val Thr Thr Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu 850 855 860	2592
tcc ttc cag aac cct ctc ttc cat atg gct gcc gat gga cca ggg ccc Ser Phe Gln Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro 865 870 875	2640

cca gca ggc cat gga ggg agc agt ggc cat ggt cca cct tcc tcc cat	2688
Pro Ala Gly His Gly Ser Ser Gly His Gly Pro Pro Ser Ser His	
880 885 890 895	
cac cac cac cac cat cac cat cac cga ggg gga gaa ccc cca ggg	2736
His His His His His His His Arg Gly Gly Glu Pro Pro Gly	
900 905 910	
gac act ttt gcc ccg ttc cat ggc tat agc aag agc gag gac ctc tct	2784
Asp Thr Phe Ala Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser	
915 920 925	
aca ggg gtc cct aag ccc cct gcg gcc tcc atc ctt cac agc cac agc	2832
Thr Gly Val Pro Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser	
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Tyr Ser Asp Glu Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln	
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Ala Arg Pro Arg Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly	
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Ser Gly Gly Ser Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile	
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Thr Lys Gln His Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro	
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 SYNGAP-B

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Ile Leu Pro Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu Met		
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Gln Ser Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser		
115 120 125		
Ser Ala Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Ile		
130 135 140		
Lys Pro Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val		
145 150 155 160		

Thr Thr Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu
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 Arg Asp Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys
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 Asp Asn Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu
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 Ala Arg Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu
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 Asp Asp Met Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala Ser
 225 230 235 240
 Gly Asp Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro
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 Ala Val Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys
 260 265 270
 Arg Lys Lys Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val
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 Ala Thr Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr
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 Leu Pro Thr Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly Gly
 305 310 315 320
 Gly Gly Ser Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys Pro
 325 330 335
 Ala Val Arg Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro Met
 340 345 350
 Glu Leu Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg Met
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 Leu Cys Ala Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu Glu
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 Asp Phe Leu Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met Glu
 405 410 415
 Arg Glu His Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala Ile
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 Glu Glu Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala Ile
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 Gly Glu Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu Val
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Asp Pro Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala Asn
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 Leu Arg Met Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser His
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 Arg Cys Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile Ser
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 Phe Thr Ser Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu Glu
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 Asp Thr Leu Thr Asn Ser Ser Phe Glu Gly Tyr Ile Asp Leu Gly
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 675 680 685
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 690 695 700
 Ile Asp Leu Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met Asp
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 Met Ala Arg Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro Pro
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 Pro Gly Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu Ala
 740 745 750
 Arg Ser Ser Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu Pro
 755 760 765

Glu Gln Lys Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp Leu
 770 775 780

Gln Gly Asp Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser Asn
 785 790 795 800

Leu Ala Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu Thr
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Ala Ala Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln Gly
 820 825 830

Ser Gly Ser Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met Gly
 835 840 845

Val Thr Thr Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu Ser
 850 855 860

Phe Gln Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro Pro
 865 870 875 880

Ala Gly His Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His His
 885 890 895

His His His His His His Arg Gly Gly Glu Pro Pro Gly Asp
 900 905 910

Thr Phe Ala Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser Thr
 915 920 925

Gly Val Pro Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser Tyr
 930 935 940

Ser Asp Glu Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln Leu
 945 950 955 960

Ser Leu Gln Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile Thr
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Ile Gly Pro Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Ser Gly
 980 985 990

Gly Gly Ser Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln Arg
 995 1000 1005

Gly Lys Ser Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg Pro
 1010 1015 1020

Ser Ser Gly Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro Ala
 1025 1030 1035 1040

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Gly Gly Ser Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile Thr
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Lys Gln His Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro Ala
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 1125 1130 1135
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 Lys Leu Glu Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln Thr
 1155 1160 1165
 Ser Lys Ile Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu Lys
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 Arg Leu Arg Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser Ile
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 Ile Gly Arg Leu Met Leu Val Glu Glu Leu Arg Arg Asp His Pro
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 Pro His Leu Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro
 1250 1255 1260
 Gly Cys Arg Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro Gln Thr Thr
 1265 1270 1275 1280
 Ser Pro Pro Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro Tyr Pro Gly
 1285 1290 1295
 Pro Pro Ser Val Thr Asp Leu Leu Pro Ser Ala Pro Asp Pro Gly Thr
 1300 1305 1310
 Ser Pro Thr Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser
 1315 1320 1325
 Pro Leu Thr Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His
 1330 1335 1340
 Ser Arg Arg Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr Pro Gly His
 1345 1350 1355 1360
 His Leu Pro His Thr Asp Pro Phe Thr Leu Gly Cys Tyr Pro His Pro
 1365 1370 1375

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 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: mammalian
 SYNGAP-C

<220>
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1 5 10 15		
cag caa ggc ttc ctg agc cgg agg cta aaa agc tcc atc aaa cgt aca		96
Gln Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile Lys Arg Thr		
20 25 30		
aag tca caa ccc aaa ctt gac cgg acc agc agc ttt cga cag atc ctg		144
Lys Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg Gln Ile Leu		
35 40 45		
cct cgc ttc cga agt gct gac cat gac cgg gcc cgg ctg atg cag agc		192
Pro Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu Met Gln Ser		
50 55 60		
ttc aag gag tct cac tcc cat gag tcc ctg ctg agt ccc agc agt gct		240
Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser Ala		
65 70 75		
gct gag gcc ctg gag ctc aac ctg gat gaa gac tcc att atc aag cca		288
Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Ile Lys Pro		
80 85 90 95		
gta cac agc tcc atc ctg ggc cag gag ttc tgc ttt gag gta aca aca		336
Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr Thr		
100 105 110		
tcg tct ggg aca aaa tgt ttt gcc tgt cgg tct gca gcc gaa agg gac		384
Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg Asp		
115 120 125		
aaa tgg att gag aat cta cag agg gct gtg aaa ccc aac aag gac aac		432
Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp Asn		
130 135 140		
agc cgc cgg gta gat aac gtg ctg aaa cta tgg atc ata gaa gct cga		480
Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu Ala Arg		
145 150 155		
gag ctg ccc ccc aag aag cga tat tac tgc gag tta tgc ctg gac gac		528
Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu Asp Asp		
160 165 170 175		

atg ctc tat gca cgg acc act tcc aag ccc cgc tca gcc tca gga gac Met Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala Ser Gly Asp 180 185 190	576
act gtc ttt tgg ggc gag cac ttc qag ttt aac aac ctg cct gct gtc Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro Ala Val 195 200 205	624
cgg gcg ctg cgg ctg cat ctg tac cgt gac tcg gac aaa aag cgg aag Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys Arg Lys 210 215 220	672
aag gac aag gca ggc tac gtt ggc ctg gtg act gtt cca gtg gcc acc Lys Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val Ala Thr 225 230 235	720
ctg gct ggg cgc cac ttc aca gag cag tgg tac ccc gtg acc ctg cca Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr Leu Pro 240 245 250 255	768
aca gga agt ggg ggc tct ggg ggt atg ggc tcg ggg gga gga ggg ggg Thr Gly Ser Gly Gly Met Gly Ser Gly Gly Gly Gly Gly 260 265 270	816
tca ggg ggc ggc tca ggg ggc aaa ggg aaa gga ggc tgt cct gct gtg Ser Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys Pro Ala Val 275 280 285	864
cgg ctg aag gcc cgt tac cag aca atg agt atc ctg ccc atg gag cta Arg Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro Met Glu Leu 290 295 300	912
tat aag gag ttt gca gaa tat gtg acc aac cac tac cgc atg ctg tgt Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg Met Leu Cys 305 310 315	960
gcc gtg ctg gag ccc gcc ctc aat gtc aag ggc aag gag gag gtc qct Ala Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu Glu Val Ala 320 325 330 335	1008
agt gca ctg gtt cac atc ctg caa agc aca ggc aag gcc aag gac ttc Ser Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala Lys Asp Phe 340 345 350	1056
ctt tca gac atg gcc atg tca gag gta gac cgg ttc atg gag gag cgg gaa Leu Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met Glu Arg Glu 355 360 365	1104
cac ctc ata ttc cgc gag aac acg ctc gcc act aaa gcc ata gaa gag His Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala Ile Glu Glu 370 375 380	1152
tat atg aga ctg att ggc cag aaa tac ctc aag gat gcc att ggg gag Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala Ile Gly Glu 385 390 395	1200

ttc atc cgg gct ctg tat gaa tct gag gag aac tgt gaa gta gac ccc Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu Val Asp Pro 400 405 410 415	1248
atc aag tgc aca gcg tcc agt ctg gca gag cac cag gcc aac ctg cgg Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala Asn Leu Arg 420 425 430	1296
atg tgc tgt gag ttg gcc ctg tgc aag gtg gtc aac tcc cat tgc gtg Met Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser His Cys Val 435 440 445	1344
ttc ccg agg gag ctg aag gag gtg ttt gca tca tgg cgg ctg cgc tgt Phe Pro Arg Glu Leu Lys Glu Val Phe Ala Ser Trp Arg Leu Arg Cys 450 455 460	1392
gca gag cgg ggc cgg gag gac att gct gac agg ctg atc agc gcc tcg Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile Ser Ala Ser 465 470 475	1440
ctc ttc ctg cgc ttc ctc tgc ccg gcc atc atg tcg ccc agt ctg ttt Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro Ser Leu Phe 480 485 490 495	1488
gga ctg atg cag gag tac cca gat gag cag acc tca cga acc ctc acc Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg Thr Leu Thr 500 505 510	1536
ctc atc gcc aag gtt atc cag aac ctg gcc aac ttt tcc aag ttt acc Leu Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser Lys Phe Thr 515 520 525	1584
tca aag gag gac ttc ctg ggc ttc atg aac gag ttt ctg gag ctg gaa Ser Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu Glu Leu Glu 530 535 540	1632
tgg ggt tct atg cag caa ttc ttg tat gag ata tcc aac ctg gac aca Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn Leu Asp Thr 545 550 555	1680
ctg acc aac agc agc agt ttt gag ggc tac ata gac ttg ggc cgc gag Leu Thr Asn Ser Ser Phe Glu Gly Tyr Ile Asp Leu Gly Arg Glu 560 565 570 575	1728
ctc tcc aca ctt cac gcc ctg ctc tgg gag gtg ctg ccc cag ctc agc Leu Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro Gln Leu Ser 580 585 590	1776
aag gaa gcc ctc ctg aag ctg ggc ccg ctg ccc cgg ctc ctc agc gac Lys Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu Leu Ser Asp 595 600 605	1824
atc agc aca gcc ctg agg aac cct aac atc caa agg cag ccg agc cgc Ile Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln Pro Ser Arg 610 615 620	1872

cac cac cat cac cat cac cga ggg gga gaa ccc cca ggg gac act ttt		2592
His His His His His Arg Gly Gly Glu Pro Pro Gly Asp Thr Phe		
850 855 860		
gcc ccg ttc cat ggc tat agc aag agc gag gac ctc tct aca ggg gtc		2640
Ala Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser Thr Gly Val		
865 870 875		
cct aag ccc cct gcg gcc tcc atc ctt cac agc cac agc tac agt gat		2688
Pro Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser Tyr Ser Asp		
880 885 890 895		
gag ttt gga ccc tct ggt act gat ttt acc cgt cgg cag ctc tca ctt		2736
Glu Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln Leu Ser Leu		
900 905 910		
cag gac aac cta cag cac atg ctc tcc ccg ccc cag atc acc atc ggt		2784
Gln Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile Thr Ile Gly		
915 920 925		
ccc cag agg cca gct ccc tca ggg cca gga ggg ggc agt ggt ggg ggc		2832
Pro Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Ser Gly Gly Gly		
930 935 940		
agt ggt ggg ggc ggt ggg ggc cag cca cct ccc ttg cag agg ggc aaa		2880
Ser Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln Arg Gly Lys		
945 950 955		
tct cag cag ttg aca gtg agt gct gcc cag aaa ccc cgg ccg tcc agc		2928
Ser Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg Pro Ser Ser		
960 965 970 975		
ggg aac cta ttg cag tcc ccg gaa cca agt tat ggt cct gcc cgt cca		2976
Gly Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro Ala Arg Pro		
980 985 990		
cgg caa cag agc ctc agc aaa gag ggc agc att ggg ggc agc ggg ggc		3024
Arg Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly Ser Gly Gly		
995 1000 1005		
agc ggt ggc gga ggg ggt ggg ggg ctc aag ccc tcc atc acc aag cag		3072
Ser Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile Thr Lys Gln		
1010 1015 1020		
cat tcc cag act cca tcc acg ctg aac ccc acg atg ccg gcc tcg gag		3120
His Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro Ala Ser Glu		
1025 1030 1035		
cgg act gta gcc tgg gtg tcc aat atg cct cac ctg tcc gct gac atc		3168
Arg Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser Ala Asp Ile		
1040 1045 1050 1055		
gag agt gca cac att gag cgg gaa gag tac aag ctg aag gag tac tcg		3216
Glu Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys Glu Tyr Ser		
1060 1065 1070		

aag tcc atg gac gag agc cga ctg gac agg gtg aag gag tac gag gag	3264
Lys Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu Tyr Glu Glu	
1075 1080 1085	
gag atc cac tca ctg aag gaa agg cta cac atg tcc aac cg ^g aag ctg	3312
Glu Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn Arg Lys Leu	
1090 1095 1100	
gaa gag tac gag cg ^g agg ctg ctg tcc cag gaa gag cag acc agc aag	3360
Glu Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln Thr Ser Lys	
1105 1110 1115	
atc ctg atg cag tac caa gcc cgc ctg gag cag agc gag aag cgc ttg	3408
Ile Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu Lys Arg Leu	
1120 1125 1130 1135	
agg cag cag cag gtg gag aag gac tcc cag atc aag agc atc att ggc	3456
Arg Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser Ile Ile Gly	
1140 1145 1150	
agg ctg atg ctg gtg gag gag ctg cgc cg ^g gac cac ccc gcc atg	3504
Arg Leu Met Leu Val Glu Glu Leu Arg Arg Asp His Pro Ala Met	
1155 1160 1165	
gct gag ccg ctg cct gaa ccc aag aag agg ctg ctc gac gct cag aga	3552
Ala Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp Ala Gln Arg	
1170 1175 1180	
ggc agc ttc ccc cct tgg gtc caa caa acc cgc gtg tga cgc tgg ccc	3600
Gly Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val Arg Trp Pro	
1185 1190 1195	
cac ctt gga acg gcc tgg ccc ccc cag ccc cac ccc ccc cac ccc ggc	3648
His Leu Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro Gly	
1200 1205 1210	
tgc aga tca cag aga acg gcg agt tcc gga aca ccg cag acc act agc	3696
Cys Arg Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro Gln Thr Thr Ser	
1215 1220 1225 1230	
cca ccc agc atc aca gac ctc ctt ccc agt gca ccc tac ccc ggc cca	3744
Pro Pro Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro Tyr Pro Gly Pro	
1235 1240 1245	
ccc agc gtc aca gac ctc ctt ccc agt gca ccc gac cct gga aca tca	3792
Pro Ser Val Thr Asp Leu Leu Pro Ser Ala Pro Asp Pro Gly Thr Ser	
1250 1255 1260	
cca acc acc agg act gga cgt cac caa ggg aca gcg gga ttg tct ccc	3840
Pro Thr Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser Pro	
1265 1270 1275	
tta acg cct cct tgg ggc acc cat ctg tca acc cca ctg ctc cat tcc	3888
Leu Thr Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His Ser	
1280 1285 1290	

agg agg gag agt ggg acc ctc agc tgc cct ctc acc cca gga cac cac	3936
Arg Arg Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr Pro Gly His His	
1295 1300 1305 1310	
ctc ccc cac aca gac ccc ttc act ctg ggg tgc tat ccc cat cct	3981
Leu Pro His Thr Asp Pro Phe Thr Leu Gly Cys Tyr Pro His Pro	
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<223> Description of Unknown Organism: mammalian	
SYNGAP-C	
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Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg Gln Ile Leu Pro	
35 40 45	
Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu Met Gln Ser Phe	
50 55 60	
Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser Ala Ala	
65 70 75 80	
Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Ile Lys Pro Val	
85 90 95	
His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr Thr Ser	
100 105 110	
Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg Asp Lys	
115 120 125	
Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp Asn Ser	
130 135 140	
Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu Ala Arg Glu	
145 150 155 160	
Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu Asp Asp Met	
165 170 175	
Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala Ser Gly Asp Thr	
180 185 190	
Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro Ala Val Arg	
195 200 205	

Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys Arg Lys Lys
 210 215 220
 Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val Ala Thr Leu
 225 230 235 240
 Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr Leu Pro Thr
 245 250 255
 Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly Gly Ser
 260 265 270
 Gly Gly Gly Ser Gly Gly Lys Gly Lys Gly Cys Pro Ala Val Arg
 275 280 285
 Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro Met Glu Leu Tyr
 290 295 300
 Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg Met Leu Cys Ala
 305 310 315 320
 Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu Glu Val Ala Ser
 325 330 335
 Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala Lys Asp Phe Leu
 340 345 350
 Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met Glu Arg Glu His
 355 360 365
 Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala Ile Glu Glu Tyr
 370 375 380
 Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala Ile Gly Glu Phe
 385 390 395 400
 Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu Val Asp Pro Ile
 405 410 415
 Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala Asn Leu Arg Met
 420 425 430
 Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser His Cys Val Phe
 435 440 445
 Pro Arg Glu Leu Lys Glu Val Phe Ala Ser Trp Arg Leu Arg Cys Ala
 450 455 460
 Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile Ser Ala Ser Leu
 465 470 475 480
 Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro Ser Leu Phe Gly
 485 490 495
 Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg Thr Leu Thr Leu
 500 505 510

Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser Lys Phe Thr Ser
 515 520 525
 Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu Glu Leu Glu Trp
 530 535 540
 Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn Leu Asp Thr Leu
 545 550 555 560
 Thr Asn Ser Ser Ser Phe Glu Gly Tyr Ile Asp Leu Gly Arg Glu Leu
 565 570 575
 Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro Gln Leu Ser Lys
 580 585 590
 Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu Leu Ser Asp Ile
 595 600 605
 Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln Pro Ser Arg Gln
 610 615 620
 Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg Gly Pro Ser Ala
 625 630 635 640
 Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser Ser Ile Asp Leu
 645 650 655
 Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met Asp Met Ala Arg
 660 665 670
 Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro Pro Gly Gly
 675 680 685
 Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu Ala Arg Ser Ser
 690 695 700
 Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu Pro Glu Gln Lys
 705 710 715 720
 Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp Leu Gln Gly Asp
 725 730 735
 Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser Asn Leu Ala Ala
 740 745 750
 Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu Thr Ala Ala Leu
 755 760 765
 Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln Gly Ser Gly Ser
 770 775 780
 Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met Gly Val Thr Thr
 785 790 795 800
 Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu Ser Phe Gln Asn
 805 810 815

Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro Pro Ala Gly His
 820 825 830
 Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His His His His His
 835 840 845
 His His His His Arg Gly Gly Glu Pro Pro Gly Asp Thr Phe Ala
 850 855 860
 Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser Thr Gly Val Pro
 865 870 875 880
 Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser Tyr Ser Asp Glu
 885 890 895
 Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln Leu Ser Leu Gln
 900 905 910
 Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile Thr Ile Gly Pro
 915 920 925
 Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Ser Gly Gly Ser
 930 935 940
 Gly Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln Arg Gly Lys Ser
 945 950 955 960
 Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg Pro Ser Ser Gly
 965 970 975
 Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro Ala Arg Pro Arg
 980 985 990
 Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly Ser Gly Gly Ser
 995 1000 1005
 Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile Thr Lys Gln His
 1010 1015 1020
 Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro Ala Ser Glu Arg
 1025 1030 1035 1040
 Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser Ala Asp Ile Glu
 1045 1050 1055
 Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys Glu Tyr Ser Lys
 1060 1065 1070
 Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu Tyr Glu Glu Glu
 1075 1080 1085
 Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn Arg Lys Leu Glu
 1090 1095 1100
 Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln Thr Ser Lys Ile
 1105 1110 1115 1120

Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu Lys Arg Leu Arg
 1125 1130 1135
 Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser Ile Ile Gly Arg
 1140 1145 1150
 Leu Met Leu Val Glu Glu Leu Arg Arg Asp His Pro Ala Met Ala
 1155 1160 1165
 Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp Ala Gln Arg Gly
 1170 1175 1180
 Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val Arg Trp Pro His Leu
 1185 1190 1195 1200
 Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro Gly Cys Arg
 1205 1210 1215
 Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro Gln Thr Thr Ser Pro Pro
 1220 1225 1230
 Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro Tyr Pro Gly Pro Pro Ser
 1235 1240 1245
 Val Thr Asp Leu Leu Pro Ser Ala Pro Asp Pro Gly Thr Ser Pro Thr
 1250 1255 1260
 Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser Pro Leu Thr
 1265 1270 1275 1280
 Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His Ser Arg Arg
 1285 1290 1295
 Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr Pro Gly His His Leu Pro
 1300 1305 1310
 His Thr Asp Pro Phe Thr Leu Gly Cys Tyr Pro His Pro
 1315 1320 1325

<210> 7
 <211> 216
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: mammalian
 SYNGAP-C

<400> 7
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 Arg Phe Met Glu Arg Glu His Leu Ile Phe Arg Glu Asn Thr Leu Ala
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Thr Lys Ala Ile Glu Glu Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu
 35 40 45
 Lys Asp Ala Ile Gly Glu Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu
 50 55 60
 Asn Cys Glu Val Asp Pro Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu
 65 70 75 80
 His Gln Ala Asn Leu Arg Met Cys Cys Glu Leu Ala Leu Cys Lys Val
 85 90 95
 Val Asn Ser His Cys Val Phe Pro Arg Glu Leu Lys Glu Val Phe Ala
 100 105 110
 Ser Trp Arg Leu Arg Cys Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp
 115 120 125
 Arg Leu Ile Ser Ala Ser Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile
 130 135 140
 Met Ser Pro Ser Leu Phe Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln
 145 150 155 160
 Thr Ser Arg Thr Leu Thr Leu Ile Ala Lys Val Ile Gln Asn Leu Ala
 165 170 175
 Asn Phe Ser Lys Phe Thr Ser Lys Glu Asp Phe Leu Gly Phe Met Asn
 180 185 190
 Glu Phe Leu Glu Leu Glu Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu
 195 200 205
 Ile Ser Asn Leu Asp Thr Leu Thr
 210 215

<210> 8
 <211> 218
 <212> PRT
 <213> Rattus norvegicus

<400> 8
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 Thr Leu Met Glu Gln Tyr Met Lys Ala Thr Ala Thr Gln Phe Val His
 35 40 45
 His Ala Leu Lys Asp Ser Ile Leu Lys Ile Met Glu Val Gln His Lys
 50 55 60
 Trp Pro Thr Asn Asn Thr Met Arg Thr Arg Val Val Ser Gly Phe Val
 65 70 75 80

Phe Leu Arg Leu Ile Cys Pro Ala Ile Leu Asn Pro Arg Met Phe Asn
 85 90 95
 Ile Ile Ser Asp Ser Pro Ser Pro Ile Ala Ala Arg Thr Leu Thr Leu
 100 105 110
 Val Ala Lys Ser Val Gln Asn Leu Ala Asn Ser Lys Gln Ser Cys Glu
 115 120 125
 Leu Ser Pro Ser Lys Leu Glu Lys Asn Glu Asp Val Asn Thr Asn Leu
 130 135 140
 Ala His Leu Leu Ser Ile Leu Ser Glu Leu Val Glu Lys Ile Phe Met
 145 150 155 160
 Ala Ser Glu Ile Leu Pro Pro Thr Leu Arg Tyr Ile Tyr Gly Cys Leu
 165 170 175
 Gln Lys Ser Leu Val Glu Phe Gly Ala Lys Glu Pro Tyr Met Glu Gly
 180 185 190
 Val Asn Pro Phe Ile Lys Ser Asn Lys His Arg Met Ile Met Phe Leu
 195 200 205
 Asp Glu Leu Gly Asn Val Pro Glu Leu Pro
 210 215

<210> 9
 <211> 219
 <212> PRT
 <213> Homo sapiens

<400> 9
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 Leu Ala Asp Ser Met Gln Thr Leu Phe Arg Gly Asn Ser Leu Ala Ser
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 Lys Ile Met Thr Phe Cys Phe Lys Val Tyr Gly Ala Thr Tyr Leu Gln
 35 40 45
 Lys Leu Leu Asp Pro Leu Leu Arg Ile Val Ile Thr Ser Ser Asp Trp
 50 55 60
 Gln His Val Ser Phe Glu Val Asp Pro Thr Arg Leu Glu Pro Ser Glu
 65 70 75 80
 Ser Leu Glu Glu Asn Gln Arg Asn Leu Leu Gln Met Thr Glu Lys Phe
 85 90 95
 Phe His Ala Ile Ile Ser Ser Ser Glu Phe Pro Pro Gln Leu Arg
 100 105 110
 Ser Val Cys His Cys Leu Tyr Gln Val Val Ser Gln Arg Phe Pro Gln
 115 120 125

Asn Ser Ile Gly Ala Val Gly Ser Ala Met Phe Leu Arg Phe Ile Asn
 130 135 140

Pro Ala Ile Val Ser Pro Tyr Glu Ala Gly Ile Leu Asp Lys Lys Pro
 145 150 155 160

Pro Pro Arg Ile Glu Arg Gly Leu Lys Leu Met Ser Lys Ile Leu Gln
 165 170 175

Ser Ile Ala Asn His Val Leu Phe Thr Lys Glu Glu His Met Arg Pro
 180 185 190

Phe Asn Asp Phe Val Lys Ser Asn Phe Asp Ala Ala Arg Arg Phe Phe
 195 200 205

Leu Asp Ile Ala Ser Asp Cys Pro Thr Ser Asp
 210 215

<210> 10

<211> 82

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: mammalian
 SYNGAP-A

<400> 10

Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser Ala
 1 5 10 15

Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Lys Lys Pro
 20 25 30

Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr Thr
 35 40 45

Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg Asp
 50 55 60

Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp Asn
 65 70 75 80

Ser Arg

<210> 11

<211> 114

<212> PRT

<213> Homo sapiens

<400> 11

Phe Tyr Lys Asn Ile Val Lys Lys Gly Tyr Leu Leu Lys Lys Gly Lys
 1 5 10 15

Gly Lys Arg Trp Lys Asn Leu Tyr Phe Ile Leu Glu Gly Ser Asp Ala
 20 25 30

Gln Leu Ile Tyr Phe Glu Ser Glu Lys Arg Ala Thr Lys Pro Lys Gly
 35 40 45

Leu Ile Asp Leu Ser Val Cys Ser Val Tyr Val Val His Asp Ser Leu
 50 55 60

Phe Gly Arg Pro Asn Cys Phe Gln Ile Val Val Gln His Phe Ser Glu
 65 70 75 80

Glu His Tyr Ile Phe Tyr Phe Ala Gly Glu Thr Pro Glu Gln Ala Glu
 85 90 95

Asp Trp Met Lys Gly Leu Gln Ala Phe Cys Asn Leu Arg Lys Ser Ser
 100 105 110

Pro Gly

<210> 12

<211> 111

<212> PRT

<213> *Drosophila melanogaster*

<400> 12

Pro Val Leu Leu Lys Glu Gly Glu Gly Leu Met Thr Lys Tyr Pro Thr
 1 5 10 15

Ser Arg Lys Arg Phe Gly Arg Gln Phe Lys Gln Arg His Phe Arg Leu
 20 25 30

Thr Thr His Ser Leu Ser Tyr Ala Lys Ser Lys Gly Lys Gln Pro Ile
 35 40 45

Cys Asp Ile Pro Leu Gln Glu Ile Ala Ser Val Glu Gln Leu Lys Asp
 50 55 60

Lys Ser Phe Lys Met Gln Asn Cys Phe Lys Ile Val His Asn Asp Arg
 65 70 75 80

Ser Leu Ile Val Gln Thr Thr Asn Cys Val Glu Glu Arg Glu Trp Phe
 85 90 95

Asp Leu Leu His Lys Ile Cys Leu Met Asn Ser Ile Arg Met Gln
 100 105 110

<210> 13

<211> 108

<212> PRT

<213> *Homo sapiens*

<400> 13

Met Glu Pro Lys Arg Ile Arg Glu Gly Tyr Leu Val Lys Lys Gly Ser
 1 5 10 15

Val Phe Asn Thr Trp Lys Pro Met Trp Val Val Leu Leu Glu Asp Gly
 20 25 30

Ile Glu Phe Tyr Lys Lys Ser Asp Asn Ser Pro Lys Gly Met Ile
 35 40 45

Pro Leu Lys Gly Ser Thr Leu Thr Ser Pro Cys Gln Asp Phe Gly Lys
 50 55 60

Arg Met Phe Val Phe Lys Ile Thr Thr Lys Gln Gln Asp His Phe
 65 70 75 80

Phe Gln Ala Ala Phe Leu Glu Glu Arg Asp Ala Trp Val Arg Asp Ile
 85 90 95

Asn Lys Ala Ile Lys Cys Ile Glu Gly Gly Gln Lys
 100 105

<210> 14

<211> 110

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: mammalian
 SYNGAP-A

<400> 14

Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu Ala Arg Glu Leu Pro
 1 5 10 15

Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu Asp Asp Met Leu Tyr
 20 25 30

Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala Ser Gly Asp Thr Val Phe
 35 40 45

Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro Ala Val Arg Ala Leu
 50 55 60

Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys Arg Lys Lys Asp Lys
 65 70 75 80

Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val Ala Thr Leu Ala Gly
 85 90 95

Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr Leu Pro Thr
 100 105 110

<210> 15

<211> 107

<212> PRT

<213> Homo sapiens

<400> 15
 Gln Val Ser Ser Leu Val Leu His Ile Glu Glu Ala His Lys Leu Pro
 1 5 10 15
 Val Lys His Phe Thr Asn Pro Tyr Cys Asn Ile Tyr Leu Asn Ser Val
 20 25 30
 Gln Val Ala Lys Thr His Ala Arg Glu Gly Gln Asn Pro Val Trp Ser
 35 40 45
 Glu Glu Phe Val Phe Asp Asp Leu Pro Pro Asp Ile Asn Arg Phe Glu
 50 55 60
 Ile Thr Leu Ser Asn Lys Thr Lys Ser Lys Asp Pro Asp Ile Leu
 65 70 75 80
 Phe Met Arg Cys Gln Leu Ser Arg Leu Gln Lys Gly His Ala Thr Asp
 85 90 95
 Glu Trp Phe Leu Leu Ser Ser His Ile Pro Leu
 100 105

<210> 16
 <211> 116
 <212> PRT
 <213> Rattus norvegicus

<400> 16
 Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr Val Gly Val Leu Gln Ala
 1 5 10 15
 Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr Ser Asp Pro Tyr Val
 20 25 30
 Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Tyr Glu Thr Lys Val
 35 40 45
 His Arg Lys Thr Leu Asn Pro Ala Phe Asn Glu Thr Phe Thr Phe Lys
 50 55 60
 Val Pro Tyr Gln Glu Leu Gly Gly Lys Thr Leu Val Met Ala Ile Tyr
 65 70 75 80
 Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile Gly Glu Val Lys Val
 85 90 95
 Pro Met Asn Thr Val Asp Leu Gly Gln Pro Ile Glu Glu Trp Arg Asp
 100 105 110
 Leu Gln Gly Gly
 115

<210> 17
 <211> 132
 <212> PRT
 <213> Bos taurus

<400> 17
 Leu Tyr Asp Gln Asp Asn Ser Ser Leu Lys Cys Thr Ile Ile Lys Ala
 1 5 10 15
 Lys Gly Leu Lys Pro Met Asp Ser Asn Gly Leu Ala Asp Pro Tyr Val
 20 25 30
 Lys Leu His Leu Leu Pro Gly Ala Ser Lys Ser Asn Lys Leu Arg Thr
 35 40 45
 Lys Thr Leu Arg Asn Thr Arg Asn Pro Ile Trp Asn Glu Thr Leu Val
 50 55 60
 Tyr His Gly Ile Thr Asp Glu Asp Met Gln Arg Lys Thr Leu Arg Ile
 65 70 75 80
 Ser Val Cys Asp Glu Asp Lys Phe Gly His Asn Glu Phe Ile Gly Glu
 85 90 95
 Thr Arg Phe Ser Leu Lys Lys Leu Lys Pro Asn Gln Arg Lys Asn Phe
 100 105 110
 Asn Ile Cys Leu Glu Arg Val Ile Pro Met Lys Arg Ala Gly Thr Thr
 115 120 125
 Gly Ser Ala Arg
 130

<210> 18
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 18
 acgcgtcgac cagagagccc cgcaag 26

<210> 19
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 19
 gaagatctag gtctatactg ggccac 26

<210> 20
 <211> 20

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 20
Lys Arg Leu Leu Asp Ala Gln Arg Gly Ser Phe Pro Pro Trp Val Gln
1 5 10 15

Gln Thr Arg Val
20

<210> 21
<211> 1135
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: mammalian
SYNGAP-C

<400> 21
Met Gln Ser Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro
1 5 10 15
Ser Ser Ala Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile
20 25 30
Ile Lys Pro Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu
35 40 45
Val Thr Thr Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala
50 55 60
Glu Arg Asp Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn
65 70 75 80
Lys Asp Asn Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile
85 90 95
Glu Ala Arg Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys
100 105 110
Leu Asp Asp Met Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala
115 120 125
Ser Gly Asp Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu
130 135 140
Pro Ala Val Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys
145 150 155 160
Lys Arg Lys Lys Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro
165 170 175

Val Ala Thr Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val
 180 185 190
 Thr Leu Pro Thr Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly
 195 200 205
 Gly Gly Gly Ser Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys
 210 215 220
 Pro Ala Val Arg Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro
 225 230 235 240
 Met Glu Leu Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg
 245 250 255
 Met Leu Cys Ala Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu
 260 265 270
 Glu Val Ala Ser Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala
 275 280 285
 Lys Asp Phe Leu Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met
 290 295 300
 Glu Arg Glu His Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala
 305 310 315 320
 Ile Glu Glu Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala
 325 330 335
 Ile Gly Glu Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu
 340 345 350
 Val Asp Pro Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala
 355 360 365
 Asn Leu Arg Met Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser
 370 375 380
 His Cys Val Phe Pro Arg Glu Leu Lys Glu Val Phe Ala Ser Trp Arg
 385 390 395 400
 Leu Arg Cys Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile
 405 410 415
 Ser Ala Ser Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro
 420 425 430
 Ser Leu Phe Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg
 435 440 445
 Thr Leu Thr Leu Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser
 450 455 460
 Lys Phe Thr Ser Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu
 465 470 475 480

Glu Leu Glu Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn
 485 490 495
 Leu Asp Thr Leu Thr Asn Ser Ser Phe Glu Gly Tyr Ile Asp Leu
 500 505 510
 Gly Arg Glu Leu Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro
 515 520 525
 Gln Leu Ser Lys Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu
 530 535 540
 Leu Ser Asp Ile Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln
 545 550 555 560
 Pro Ser Arg Gln Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg
 565 570 575
 Gly Pro Ser Ala Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser
 580 585 590
 Ser Ile Asp Leu Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met
 595 600 605
 Asp Met Ala Arg Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro
 610 615 620
 Pro Pro Gly Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu
 625 630 635 640
 Ala Arg Ser Ser Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu
 645 650 655
 Pro Glu Gln Lys Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp
 660 665 670
 Leu Gln Gly Asp Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser
 675 680 685
 Asn Leu Ala Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu
 690 695 700
 Thr Ala Ala Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln
 705 710 715 720
 Gly Ser Gly Ser Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met
 725 730 735
 Gly Val Thr Thr Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu
 740 745 750
 Ser Phe Gln Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro
 755 760 765
 Pro Ala Gly His Gly Ser Ser Gly His Gly Pro Pro Ser Ser His
 770 775 780

His His His His His His His His Arg Gly Gly Glu Pro Pro Gly
 785 790 795 800
 Asp Thr Phe Ala Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser
 805 810 815
 Thr Gly Val Pro Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser
 820 825 830
 Tyr Ser Asp Glu Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln
 835 840 845
 Leu Ser Leu Gln Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile
 850 855 860
 Thr Ile Gly Pro Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Ser
 865 870 875 880
 Gly Gly Gly Ser Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln
 885 890 895
 Arg Gly Lys Ser Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg
 900 905 910
 Pro Ser Ser Gly Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro
 915 920 925
 Ala Arg Pro Arg Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly
 930 935 940
 Ser Gly Gly Ser Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile
 945 950 955 960
 Thr Lys Gln His Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro
 965 970 975
 Ala Ser Glu Arg Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser
 980 985 990
 Ala Asp Ile Glu Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys
 995 1000 1005
 Glu Tyr Ser Lys Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu
 1010 1015 1020
 Tyr Glu Glu Glu Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn
 1025 1030 1035 1040
 Arg Lys Leu Glu Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln
 1045 1050 1055
 Thr Ser Lys Ile Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu
 1060 1065 1070
 Lys Arg Leu Arg Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser
 1075 1080 1085

Ile Ile Gly Arg Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His
1090 1095 1100

Pro Ala Met Ala Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp
1105 1110 1115 1120

Ala Gln Arg Gly Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val
1125 1130 1135

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